

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/319,745DATE: 10/24/94  
TIME: 10:56:56

INPUT SET: S604.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERED

## (1) General Information:

(i) APPLICANT: Scott, Matthew P.  
Goodrich, Lisa V.  
Johnson, Ronald L.

(ii) TITLE OF INVENTION: Mammalian Patched Gene and Its Use

(iii) NUMBER OF SEQUENCES: 20

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert  
(B) STREET: 4 Embarcadero Center, Suite 3400  
(C) CITY: San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94111-4187

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Rowland, Bertram I  
(B) REGISTRATION NUMBER: 20,015  
(C) REFERENCE/DOCKET NUMBER: A60190/BIR STAN171

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 781-1989  
(B) TELEFAX: (415) 398-3249  
(C) TELEX: 910277299

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 680 base pairs

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47 (B) TYPE: nucleic acid  
48 (C) STRANDEDNESS: single  
49 (D) TOPOLOGY: linear  
50

51 (ii) MOLECULE TYPE: cDNA  
52  
53  
54

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
56

57 AACCTATGGC ACCCCCCCCA ACCTTTCCTA ACAAACCCC TTTATACCCC CTTAAATTTT 60  
58  
59 CCACCCAAAC CCTGAACAGA AACCTTTTTA ACCCCCCCCA CCCGGAATTC CATCCCCCCC 120  
60  
61 AAATTACAAC TCCAGCCAAA ATTAAAATTG GTCCTAACCT AACCATGTTG TTACGGTTTC 180  
62  
63 CCCCCCAAAA TACATGCACT GGCCCGAACA CTTGATCGTT GCCGTTCCTA TAAGAATAAA 240  
64  
65 TCTGGTCATA TTAAACAAGC CAAAGCTTTA CAACTGTTG TACAATTAAT GGGCGAACAC 300  
66  
67 GAACTGTTTC AATTCTGGTC TGGACATTAC AAAGTGCACC ACATCGGATG GAACCAGGAG 360  
68  
69 AAGGCCACAA CCGTACTGAA CGCCTGGCAG AAGAAGTTCG CACAGGTTGG TGGTTGGCGC 420  
70  
71 AAGGAGTAGA GTGAATGGTG GTAATTTTTG GTTGTTCAG GAGGTGGATC GTCTGACGAA 480  
72  
73 GAGCAAGAAG TCGTCGAATT ACATCTTCGT GACGTTCTCC ACCGCCAATT TGAACAAGAT 540  
74  
75 GTTGAAGGAG GCGTCGAAAC GGACGTGGTG AAGCTGGGGG TGGTGCTGGG GGTGGCGGCG 600  
76  
77 GTGTACGGGT GGGTGGCCCA GTCGGGGCTG GCTGCCTTGG GAGTGCTGGT CTTGCGGCTC 660  
78  
79 ATTCGCCCTA TAGTAGCGTA 680  
80

81 (2) INFORMATION FOR SEQ ID NO:2:  
82

83 (i) SEQUENCE CHARACTERISTICS:  
84 (A) LENGTH: 107 amino acids  
85 (B) TYPE: amino acid  
86 (C) STRANDEDNESS: single  
87 (D) TOPOLOGY: linear  
88

89 (ii) MOLECULE TYPE: protein  
90  
91  
92

93 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
94

95 Xaa Pro Pro Pro Asn Tyr Asn Ser Xaa Pro Lys Xaa Xaa Xaa Leu Val  
96 1 5 10 15  
97  
98 Leu Thr Pro Xaa Val Val Thr Val Ser Pro Pro Lys Tyr Met His Trp  
99 20 25 30

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100
101   Pro Glu His Leu Ile Val Ala Val Pro Ile Arg Ile Asn Leu Val Ile
102           35                     40                     45
103
104   Leu Asn Lys Pro Lys Ala Leu Gln Thr Val Val Gln Leu Met Gly Glu
105           50                     55                     60
106
107   His Glu Leu Phe Glu Phe Trp Ser Gly His Tyr Lys Val His His Ile
108           65                     70                     75                     80
109
110   Gly Trp Asn Gln Glu Lys Ala Thr Thr Val Leu Asn Ala Trp Gln Lys
111           85                     90                     95
112
113   Lys Phe Ala Gln Val Gly Gly Trp Arg Lys Glu
114           100                    105
115

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

130  GGCCAGTGTC GACACGCTGT TAAGGTGTTA CGAAACTATC GAAACTCTGT ACCGTTCCGT      60
131
132  GTTACATTCG GTCAGTGATA AACAGAAGTG AATAATTCGG GTGTACAAGT GTGTGGTTAT      120
133
134  GTGGCGGCCG GTGATATGAC AGCGTGCGCC GCCAGACGGA TTCCAGCCGT CTTTCATGAGG      180
135
136  ATATCGGTGA CAAGCCTGGC CCCGAGATCA TGGTGGCTCC CGATTCCGAG GCTCCTTCGA      240
137
138  ATCCTCGGAT AACGGCTGCA CACGAGAGCC CCTGCGCCAC CGAGGCGCGC CACAGTGCTG      300
139
140  ATCTTTACAT ACGTACCAGT TGGGTGGACG CCGCACTAGC TCTCTCTGAA CTCGAAAAGG      360
141
142  GTAACATCGA AGGAGGAAGA ACCTCTCTGT GGATACGAGC GTGGCTACAA GAACAGCTCT      420
143
144  TTATTTTGGG CTGCTTTCTT CAAGGCGACG CGGGGAAAGT CCTCTTCGTT GCCATCCTCG      480
145
146  TTCTGTCGAC GTTCTGCGTC GGTCTCAAGT CAGCACAAAT ACATACAAGG GTCGACCAAC      540
147
148  TCTGGGTTCA AGAGGGTGGT AGATTAGAAG CCGAGTTGAA ATATACAGCG CAAGCTTTGG      600
149
150  GCGAGGCGGA CTCCTCGACG CACCAGCTTG TCATACAAAC TGCCAAAGAT CCAGACGTCT      660
151
152  CCCTGCTACA TCCAGGCGCG TTGCTTGAAC ACCTTAAGGT GGTGCACGCA GCGACTCGGG      720

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153							
154	TGACAGTTCA	CATGTACGAC	ATTGAGTGGC	GCCTCAAAGA	CCTGTGCTAC	AGCCCCAGCA	780
155							
156	TACCGGACTT	CGAGGGTTAC	CACCACATCG	AGTCAATCAT	AGACAACGTC	ATCCCCTGCG	840
157							
158	CTATTATCAC	CCCCCTTGAT	TGCTTCTGGG	AAGGCTCCAA	GTTGCTTGGT	CCCGATTATC	900
159							
160	CTATATACGT	ACCACATCTT	AAACACAAAC	TACAATGGAC	ACATTTAAAT	CCATTGGAAG	960
161							
162	TTGTAGAAGA	AGTGAAAAAA	TTAAAGTTCC	AATTTCTCT	GAGCACAATA	GAGGCGTACA	1020
163							
164	TGAAGAGAGC	CGGCATCACT	TCCGCCTACA	TGAAAAAGCC	GTGCTTAGAC	CCCACCGACC	1080
165							
166	CACATTGTCC	AGCCACGGCT	CCAAACAAAA	AGTCTGGTCA	TATTCCAGAT	GTAGCGGCGG	1140
167							
168	AGCTGTCGCA	CGGATGTTAT	GGTTTCGCGG	CAGCTTACAT	GCAC TGGCCG	GAACAGTTAA	1200
169							
170	TTGTAGGGGG	AGCTACAAGG	AATTCGACAT	CAGCTCTGAG	AAAAGCACGC	GTTTACAGAC	1260
171							
172	TGTAGTACAG	TTAATGGGCG	AGAGAGAAAT	GTACGAGTAC	TGGGCCGATC	ATTATAAAGT	1320
173							
174	ACATCAAATT	GGCTGGAATC	AAGAGAAGGC	AGCTGCTGTA	CTGGATGCCT	GGCAGAGAAA	1380
175							
176	GTTTGCCGCT	GAAGTCAGAA	AAATTACTAC	CTCAGGATCA	GTATCATCGG	CTTATAGTTT	1440
177							
178	CTATCCGTTC	TCCACCTCGA	CACTTAATGA	CATACTCGGG	AAGTTCTCCG	AAGTGTCACT	1500
179							
180	GAAGAACATT	ATATTAGGCT	ATATGTTTAT	GTTAATTTAT	GTTGCCGTTA	CTTTAATACA	1560
181							
182	ATGGCGGGAT	CCGATTCGCT	CGCAAGCGGG	TGTGGGTATC	GCCGGAGTTC	TACTACTATC	1620
183							
184	AATCACTGTT	GCCGCTGGCT	TAGGATTTTG	TGCTTTATTA	GGCATACCAT	TCAACGCTTC	1680
185							
186	AAGTACGCAA	ATAGTACCAT	TCCTAGCGCT	CGGGTTAGGA	GTTCAAGATA	TGTTTCTTCT	1740
187							
188	CACTCACACG	TATGTGGAGC	AAGCGGGAGA	TGTGCCTAGA	GAAGAGAGGA	CTGGACTTGT	1800
189							
190	ATTGAAAAAG	AGCGGTTTAA	GCGTACTTCT	GGCGTCTTTG	TGCAACGTGA	TGGCATTTTT	1860
191							
192	GGCAGCAGCC	CTTCTACCTA	TTCCAGCTTT	CAGAGTATTT	TGCC TACAGG	CTGCCATACT	1920
193							
194	TCTTCTGTTT	AACTTGGGGT	CAATATTACT	GGTTTTTCCCT	GCTATGATCT	CGTTAGACCT	1980
195							
196	GCGACGGAGG	TCAGCCGCGA	GGGCCGATCT	TTTATGCTGT	TTGATGCCTG	AGAGTCCATT	2040
197							
198	ACCGAAGAAG	AAAATTCCGG	AAAGAGCAAA	AACTAGAAAA	AACGATAAGA	CTCATAGGAT	2100
199							
200	AGACACCACG	AGACAACCTC	TAGACCCAGA	TGTGTCCGAG	AACGTGACCA	AACTTGCTG	2160
201							
202	CTTAAGCGTC	TCGCTCACCA	AGTGGGCCAA	GAACCAATAC	GCGCCGTTCA	TCATGCGCCC	2220
203							
204	CGCTGTTAAG	GTTACATCCA	TGTTAGCGTT	GATTGCTGTT	ATTCTGACTA	GCGTTTGGGG	2280
205							

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206	AGCGACAAAA	GTAAAGGATG	GATTGGATTT	GACTGATATT	GTACCGGAGA	ATACAGACGA	2340
207							
208	ACACGAATTT	TTATCTCGTC	AGGAAAAATA	CTTTGGCTTC	TATAATATGT	ACGCCGTGAC	2400
209							
210	GCAAGGCAAC	TTTGAATATC	CCACCAATCA	GAAGTTATTA	TATGAGTATC	ACGATCAATT	2460
211							
212	CGTCAGAATA	CCTAATATAA	TCAAGAATGA	TAACGGCGGT	CTCACGAAAT	TTTGGTTGAG	2520
213							
214	TTTATTCCGC	GACTGGTTAT	TGGACTTGCA	AGTGGCTTTT	GATAAGGAGG	TTGCCAGCGG	2580
215							
216	TTGTATAACA	CAAGAGTATT	GGTGCAAAAA	CGCGAGTGAC	GAAGGAATAT	TGGCCTATAA	2640
217							
218	ACTTATGGTG	CAGACTGGCC	ATGTGGACAA	TCCAATCGAT	AAGTCTCTGA	TTACGGCAGG	2700
219							
220	TCACAGACTA	GTTGACAAAG	ACGGTATTAT	AAATCCAAAG	GCATTTTATA	ATTACCTATC	2760
221							
222	AGCTTGGGCT	ACTAACGACG	CGTTGGCATA	CGGAGCCTCA	CAAGGGAAC	TGAAACCTCA	2820
223							
224	GCCCCAAAGA	TGGATCCATT	CTCCGGAGGA	TGTACATTTA	GAAATAAAGA	AATCGTCGCC	2880
225							
226	ATTAATTTAC	ACACAGTTAC	CATTCTACCT	TTCCGGTCTC	AGCGACACTA	TAGCATCAAA	2940
227							
228	ACGTTGATAA	GATCTGTGCG	AGATTTATGT	CTGAAGTACG	AGGCGAAAGG	TTTACCGAAC	3000
229							
230	TTTCCATCGG	GTATACCATT	CCTTTTCTGG	GAACAGTATT	TGTATTTAAG	GACATCTTTA	3060
231							
232	CTACTGGCTT	TGGCGTGTGC	TTTGGCAGCT	GTCTTCATTG	CGGTTATGGT	GCTATTGTTG	3120
233							
234	AACGCCTGGG	CAGCAGTACT	GGTGACATTA	GCGCTGGCTA	CATTAGTACT	GCAGCTGTTA	3180
235							
236	GGTGTATGGC	CTTATTGGGC	GTGAAGCTAT	CTGCAATGCC	GGCCGTACTA	CTGGTGCTAG	3240
237							
238	CCATTGGGAG	AGGAGTTCAC	TTCACTGTGC	ATTTATGTTT	GGGTTTGTGA	ACATCAATCG	3300
239							
240	GTTGCAAGCG	GCGCCGCGCG	TCACTAGCTC	TAGAATCAGT	TCTGGCGCCA	GTGGTGACAG	3360
241							
242	GCGCTCTGGC	GGCCGCGCTG	GCTGCCTCGA	TGCTAGCTGC	AAGTGAATGT	GGCTTCGTTG	3420
243							
244	CCAGACTGTT	CTTGAGGTTA	CTACTGGACA	TCGTGTTTCT	GGGACTCATC	GATGGGTTGC	3480
245							
246	TGTTCTTCCC	TATTGTCCTT	TCGATATTGG	GACCGGCTGC	TGAGGTACGA	CCTATAGAGC	3540
247							
248	ATCCAGAACG	CTTATCGACT	CCATCGCCAA	AATGTTTCGCC	CATCCACCCT	CGCAAATCAA	3600
249							
250	GTTCCAGCTC	AGGCGGTGGT	GATAAATCAA	GTCGAACCAG	TAAATCAGCA	CCAAGGCCTT	3660
251							
252	GCGCACCATC	TCTCACGACC	ATTACTGAAG	AGCCTTCGAG	TTGGCACAGT	TCCGCCCAC	3720
253							
254	CCGTACAATC	TTCTATGCAG	TCGATAGTGG	TCCAGCCGGA	GGTGGTGGTC	GAAACTACCA	3780
255							
256	CGTATAATGG	CAGCGATTCT	GCTTCAGGAC	GGTCGACGCC	TACAAAGTCT	TCACACGGTG	3840
257							
258	GTGCTATCAC	AACTACTAAG	GTGACCGCCA	CGGCAAATAT	AAAGGTAGAA	GTGGTGACAC	3900

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/319,745**

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Original Text